

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Davis, Roger J.  
Raingeaud, Joel  
Gupta, Shashi  
Derijard, Benoit

(ii) TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-  
ACTIVATED HUMAN PROTEIN KINASE KINASES

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fish & Richardson P.C.  
(B) STREET: 225 Franklin Street  
(C) CITY: Boston  
(D) STATE: Massachusetts  
(E) COUNTRY: USA  
(F) ZIP: 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WordPerfect 5.1

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/446,083  
(B) FILING DATE: 05/19/95

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Fasse, J. Peter  
(B) REGISTRATION NUMBER: 32,983  
(C) REFERENCE/DOCKET NUMBER: 04020/09001

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 542-5070  
(B) TELEFAX: (617) 542-8906

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2030 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGCTGGCAA	TGGCCTTGCT	GACCTCGAGC	CGGGCCCACG	TGGGGACCTT	TGGAGCACAG	60
CCTACGATCC	TGGTGCAAGG	CCGGTGGATG	CAGAGGCCAG	TCCATATACC	ACCCAGGCCT	120
GCGAGGAGCG	TGGTCCCCAC	CCATCCAGCC	CATATGTGCA	AGTGCCCTTG	ACAGAGAGGC	180
TGGTCATATC	CATGGTGACC	ATTTATGGGC	CACAACAGGT	CCCCATCTGC	GCAGTGAACC	240
CTGTGCTGAG	CACCTTGCAG	ACGTGATCTT	GCTTCGTCTT	GCAGCACTGT	GCGGGGCAGG	300
AAAATCCAAG	AGGAAGAAGG	ATCTACGGAT	ATCCTGCATG	TCCAAGCCAC	CCGCACCCAA	360
CCCCACACCC	CCCCGGAACC	TGGACTCCCG	GACCTTCATC	ACCATTGGAG	ACAGAAACTT	420
TGAGGTGGAG	GCTGATGACT	TGGTGACCAT	CTCAGAACTG	GGCCGTGGAG	CCTATGGGGT	480
GGTAGAGAAG	GTGCGGCACG	CCCAGAGCGG	CACCATCATG	GCCGTGAAGC	GGATCCGGGC	540
CACCGTGAAC	TCACAGGAGC	AGAAGCGGCT	GCTCATGGAC	CTGGACATCA	ACATGCGCAC	600
GGTCGACTGT	TTCTACACTG	TCACCTTCTA	CGGGGCACTA	TTCAGAGAGG	GAGACGTGTG	660
GATCTGCATG	GAGCTCATGG	ACATCCTTGG	GGACAAGTTC	TACCGGAAGG	TGCTGGATAA	720
AAACATGACA	ATTCCAGAGG	ACATCCTTGG	GGAGATTGCT	GTGTCTATCG	TGCGGGCCCT	780
GGAGCATCTG	CACAGCAAGC	TGTCGGTGAT	CCACAGAGAT	GTGAAGCCCT	CCAATGTCCT	840
TATCAACAAG	GAGGGCCATG	TGAAGATGTG	TGACTTTGGC	ATCAGTGGCT	ACTTGGTGGA	900
CTCTGTGGCC	AAGACGATGG	ATGCCGGCTG	CAAGCCCCTAC	ATGGCCCCTG	AGAGGATCAA	960
CCCAGAGCTG	AACCAGAAGG	GCTACAATGT	CAAGTCCGAC	GTCTGGAGCC	TGGGCATCAC	1020
CATGATTGAG	ATGGCCATCC	TGCGGTTCCC	TTACGAGTCC	TGGGGGACCC	CGTTCCAGCA	1080
GCTGAAGCAG	GTGGTGGAGG	AGCCGTCCCC	CCAGCTCCCA	GCCGACCGTT	TCTCCCCCGA	1140
TTTTGTGGAC	TTCCTGCTC	AGTGCCTGAG	GAAGAACCCC	GCAGAGCGTA	TGAGCTACCT	1200
GGAGCTGATG	GAGCACCCTT	TCTTCACCTT	GCACAAAACC	AAGAAGACGG	ACATTGCTGC	1260
CTTCGTGAAG	AAGATCCTGG	GAGAAGACTC	ATAGGGGCTG	GGCCTCGGAC	CCCACTCCGG	1320
CCCTCCAGAG	CCCCACAGCC	CCATCTGCGG	GGGCAGTGCT	CACCCACACC	ATAAGCTACT	1380
GCCATCCTGG	CCCAGGGCAT	CTGGGAGGAA	CCGAGGGGGC	TGCTCCCACC	TGGCTCTGTG	1440
GCGAGCCATT	TGTCCCAAGT	GCCAAAGAAG	CAGACCATTG	GGGCTCCCAG	CCAGGCCCTT	1500
GTCGGCCCCA	CCAGTGCCTC	TCCCTGCTGC	TCCTAGGACC	CGTCTCCAGC	TGCTGAGATC	1560
CTGGACTGAG	GGGGCCTGGA	TGCCCCCTGT	GGATGCTGCT	GCCCCCTGCAC	AGCAGCTGTC	1620
CAGTGCCTGG	GTGGATGGGC	CACCGCCTTG	CCCAGCCTGG	ATGCCATCCA	AGTTGTATAT	1680
TTTTTTAATC	TCTCGACTGA	ATGGACTTTG	CACACTTTGG	CCCAGGGTGG	CCACACCTCT	1740
ATCCCGGCTT	TGGTGCGGGG	TACACAAGAG	GGGATGAGTT	GTGTGAATAC	CCCAAGACTC	1800
CCATGAGGGA	GATGCCATGA	GCCGCCCAAG	GCCTTCCCCT	GGCACTGGCA	AACAGGGCCT	1860
CTGCGGAGCA	CACTGGCTCA	CCCAGTCCTG	CCCGCCACCG	TTATCGGTGT	CATTACCTT	1920
TCGTGTTTTT	TTTAATTTAT	CCTCTGTTGA	TTTTTTCTTT	TGCTTTATGG	GTTTGGCTTG	1980
TTTTTCTTGC	ATGGTTTGA	GCTGATCGCT	TCTCCCCCAC	CCCCTAGGGG		2030

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids

(B) TYPE: peptide

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Lys	Pro	Pro	Ala	Pro	Asn	Pro	Thr	Pro	Pro	Arg	Asn	Leu	Asp
			20				25						30		
Ser	Arg	Thr	Phe	Ile	Thr	Ile	Gly	Asp	Arg	Met	Phe	Glu	Val	Glu	Ala
		35				40						45			
Asp	Asp	Leu	Val	Thr	Ile	Ser	Glu	Leu	Gly	Arg	Gly	Ala	Tyr	Gly	Val
	50					55					60				

Val	Glu	Lys	Val	Arg	His	Ala	Gln	Ser	Gly	Thr	Ile	Met	Ala	Val	Lys
65					70					75					80
Arg	Ile	Arg	Ala	Thr	Val	Asn	Ser	Gln	Glu	Gln	Lys	Arg	Leu	Leu	Met
			85						90					95	
Asp	Leu	Asp	Ile	Asn	Met	Arg	Thr	Val	Asp	Cys	Phe	Tyr	Thr	Val	Thr
			100					105					110		
Phe	Tyr	Gly	Ala	Leu	Phe	Arg	Glu	Gly	Asp	Val	Trp	Ile	Cys	Met	Glu
		115					120					125			
Leu	Met	Asp	Thr	Ser	Leu	Asp	Lys	Phe	Tyr	Arg	Lys	Val	Leu	Asp	Lys
		130				135					140				
Asn	Met	Thr	Ile	Pro	Glu	Asp	Ile	Leu	Gly	Glu	Ile	Ala	Val	Ser	Ile
145					150					155					160
Val	Arg	Ala	Leu	Glu	His	Leu	His	Ser	Lys	Leu	Ser	Val	Ile	His	Arg
				165					170					175	
Asp	Val	Lys	Pro	Ser	Asn	Val	Leu	Ile	Asn	Lys	Glu	Gly	His	Val	Lys
			200					205					210		
Met	Cys	Asp	Phe	Gly	Ile	Ser	Gly	Tyr	Leu	Val	Asp	Ser	Val	Ala	Lys
		215					220					225			
Thr	Met	Asp	Ala	Gly	Cys	Lys	Pro	Tyr	Met	Ala	Pro	Glu	Arg	Ile	Asn
		230				235					240				
Pro	Glu	Leu	Asn	Gln	Lys	Gly	Tyr	Asn	Val	Lys	Ser	Asp	Val	Trp	Ser
245					250					255					260
Leu	Gly	Ile	Thr	Met	Ile	Glu	Met	Ala	Ile	Leu	Arg	Phe	Pro	Tyr	Glu
			265					270						275	
Ser	Trp	Gly	Thr	Pro	Phe	Gln	Gln	Leu	Lys	Gln	Val	Val	Glu	Glu	Pro
			280					285					290		
Ser	Pro	Gln	Leu	Pro	Ala	Asp	Arg	Phe	Ser	Pro	Glu	Phe	Val	Asp	Phe
		295					300					305			
Thr	Ala	Gln	Cys	Leu	Arg	Lys	Asn	Pro	Ala	Glu	Arg	Met	Ser	Tyr	Leu
		310				315					320				
Glu	Leu	Met	Glu	His	Pro	Phe	Phe	Thr	Leu	His	Lys	Thr	Lys	Lys	Thr
325					330					335			338		
Asp	Ile	Ala	Ala	Phe	Val	Lys	Lys	Ile	Leu	Gly	Glu	Asp	Ser		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TAGCTGCAGC	ACAGCCTTCC	CTAACGTTGC	AACTGGGGGA	AAAATCACTT	TCCAGTCTGT	60
TTTGCAAGGT	GTGCATTTCC	ATCTTGATTC	CCTGAAAGTC	CATCTGCTGC	ATCGGTCAAG	120
AGAAACTCCA	CTTGCAATGA	GATTGCACGC	CTGCAGCTTG	CATCTTTGTT	GCAAACTAG	180
CTACAGAAGA	GAAGCAAGGC	AAAGTCTTTT	GTGCTCCCT	CCCCCATCAA	AGGAAAGGGG	240
AAAATGTCTC	AGTCGAAAGG	CAAGAAGCGA	AACCCTGGCC	TTAAAATTCC	AAAAGAAGCA	300
TTTGAACAAC	CTCAGACCAG	TTCCACACCA	CCTAGAGATT	TAGACTCCAA	GGCTTGCATT	360
TCTATTGGAA	ATCAGAACTT	TGAGGTGAAG	GCAGATGACC	TGGAGCCTAT	AATGGAAGTG	420

GGACGAGGTG	CGTACGGGGT	GGTGGAGAAG	ATGCGGCACG	TGCCCAGCGG	GCAGATCATG	480
GCACTGAAGC	GGATCCGAGC	CACAGTAAAT	AGCCAGGAAC	AGAAACGGCT	ACTGATGGAT	540
TTGGATATTT	CCATGAGGAC	GGTGGACTGT	CCATTCACTG	TCACCTTTTA	TGGCGCACTG	600
TTTCGGGAGG	GTGATGTGTG	GATCTGCATG	GAGCTCATGG	ATACATCACT	AGATAAATTC	660
TACAAACAAG	TTATTGATAA	AGGCCAGACA	ATTCCAGAGG	ACATCTTAGG	GAAAATAGCA	720
GTTTCTATTG	TAAAAGCATT	AGAACATTTA	CATAGTAAGC	TGTCTGTCAT	TCACAGAGAC	780
GTCAAGCCTT	CTAATGTACT	CATCAATGCT	CTCGGTCAAG	TGAAGATGTG	CGATTTTGGA	840
ATCAGTGGCT	ACTTGGTGGA	CTCTGTTGCT	AAAACAATTG	ATGCAGGTTG	CAAACCATAC	900
ATGGCCCCTG	AAAGAATAAA	CCCAGAGCTC	AACCAGAAGG	GATACAGTGT	GAAGTCTGAC	960
ATTTGGAGTC	TGGGCATCAC	GATGATTGAG	TTGGCCATCC	TTCGATTTCC	CTATGATTCA	1020
TGGGGAACCTC	CATTTTCAGCA	GCTCAAACAG	GTGGTAGAGG	AGCCATCGCC	ACAACTCCCA	1080
GCAGACAAGT	TCTCTGCAGA	GTTTGTGAC	TTTACCTCAC	AGTGCTTAAA	GAAGAATTCC	1140
AAAGAACGGC	CTACATACCC	AGAGCTAATG	CAACATCCAT	TTTTCACCTT	ACATGAATCC	1200
AAAGGAACAG	ATGTGGCATC	TTTTGTAAAA	CTGATTCTTG	GAGACTAAAA	AGCAGTGGAC	1260
TTAATCGGTT	GACCCTACTG	TGGATTGGTG	GGTTTCGGGG	TGAAGCAAGT	TCACTACAGC	1320
ATCAATAGAA	AGTCATCTTT	GAGATAATTT	AACCCTGCCT	CTCAGAGGGT	TTTCTCTCCC	1380
AATTTTCTTT	TTACTCCCCC	TCTTAAGGGG	GCCTTGGAAT	CTATAGTATA	GAATGAACCTG	1440
TCTAGATGGA	TGAATTATGA	TAAAGGCTTA	GGACTTCAAA	AGGTGATTAA	ATATTTAATG	1500
ATGTGTCATA	TGAGTCCTCA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1560
AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AA		1602

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 amino acids

(B) TYPE: peptide

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

				5					10					15					
Met	Ser	Gln	Ser	Lys	Gly	Lys	Lys	Arg	Asn	Pro	Gly	Leu	Lys	Ile	Pro				
			20					25					30						
Lys	Glu	Ala	Phe	Glu	Gln	Pro	Gln	Thr	Ser	Ser	Thr	Pro	Pro	Arg	Asp				
		35					40					45							
Leu	Asp	Ser	Lys	Ala	Cys	Ile	Ser	Ile	Gly	Asn	Gln	Asn	Phe	Glu	Val				
	50				55				60										
Lys	Ala	Asp	Asp	Leu	Glu	Pro	Ile	Met	Glu	Leu	Gly	Arg	Gly	Ala	Tyr				
65				70					75					80					
Gly	Val	Val	Glu	Lys	Met	Arg	His	Val	Pro	Ser	Gly	Gln	Ile	Met	Ala				
			85					90					95						
Val	Lys	Arg	Ile	Arg	Ala	Thr	Val	Asn	Ser	Gln	Glu	Gln	Lys	Arg	Leu				
		100					105						110						
Leu	Met	Asp	Leu	Asp	Ile	Ser	Met	Arg	Thr	Val	Asp	Cys	Pro	Phe	Thr				
	115				120						125								
Val	Thr	Phe	Tyr	Gly	Ala	Leu	Phe	Arg	Glu	Gly	Asp	Val	Trp	Ile	Cys				
130					135						140								
Met	Glu	Leu	Met	Asp	Thr	Ser	Leu	Asp	Lys	Phe	Tyr	Lys	Gln	Val	Ile				
145				150				155					160						
Asp	Lys	Gly	Gln	Thr	Ile	Pro	Glu	Asp	Ile	Leu	Gly	Lys	Ile	Ala	Val				

Ser	Ile	Val	Lys	Ala	Leu	Glu	His	Leu	His	Ser	Lys	Leu	Ser	Val	Ile
			180					185					190		
His	Arg	Asp	Val	Lys	Pro	Ser	Asn	Val	Leu	Ile	Asn	Ala	Leu	Gly	Gln
		195					200					205			
Val	Lys	Met	Cys	Asp	Phe	Gly	Ile	Ser	Gly	Tyr	Leu	Val	Asp	Ser	Val
	210					215					220				
Ala	Lys	Thr	Ile	Asp	Ala	Gly	Cys	Lys	Pro	Tyr	Met	Ala	Pro	Glu	Arg
225					230					235				240	
Ile	Asn	Pro	Glu	Leu	Asn	Gln	Lys	Gly	Tyr	Ser	Val	Lys	Ser	Asp	Ile
			245					250						255	
Trp	Ser	Leu	Gly	Ile	Thr	Met	Ile	Glu	Leu	Ala	Ile	Leu	Arg	Phe	Pro
		260						265					270		
Tyr	Asp	Ser	Trp	Gly	Thr	Pro	Phe	Gln	Gln	Leu	Lys	Gln	Val	Val	Glu
	275						280					285			
Glu	Pro	Ser	Pro	Gln	Leu	Pro	Ala	Asp	Lys	Phe	Ser	Ala	Glu	Phe	Val
	290					295					300				
Asp	Phe	Thr	Ser	Gln	Cys	Leu	Lys	Lys	Asn	Ser	Lys	Glu	Arg	Pro	Thr
305					310					315				320	
Tyr	Pro	Glu	Leu	Met	Gln	His	Pro	Phe	Phe	Thr	Leu	His	Glu	Ser	Lys
			325					330					334		
Gly	Thr	Asp	Val	Ala	Ser	Phe	Val	Lys	Leu	Ile	Leu	Gly	Asp		

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTAGGGTCCC	CGGCGCCAGG	CCACCCGGCC	GTCAGCAGCA	TGCAGGGTAA	ACGCAAAGCA	60
CTGAAGTTGA	ATTTTGCAAA	TCCACCTTTC	AAATCTACAG	CAAGGTTTAC	TCTGAATCCC	120
AATCCTACAG	GAGTTCAAAA	CCCACACATA	GAGAGACTGA	GAACACACAG	CATTGAGTCA	180
TCAGGAAAAC	TGAAGATCTC	CCCTGAACAA	CACTGGGATT	TCACTGCAGA	GGACTTGAAA	240
GACCTTGGAG	AAATTGGACG	AGGAGCTTAT	GGTTCTGTCA	ACAAAATGGT	CCACAAACCA	300
AGTGGGCAAA	TAATGGCAGT	TAAAAGAATT	CGGTCAACAG	TGGATGAAAA	AGAACAAAAA	360
CAACTTCTTA	TGGATTTGGA	TGTAGTAATG	CGGAGTAGTG	ATTGCCCATA	CATTGTTCAG	420
TTTTATGGTG	CACTCTTCAG	AGAGGGTGAC	TGTTGGATCT	GTATGGAAct	CATGTCTACC	480
TCGTTTGATA	AGTTTTACAA	ATATGTATAT	AGTGTATTAG	ATGATGTTAT	TCCAGAAGAA	540
ATTTTAGGCA	AAATCACTTT	AGCAACTGTG	AAAGCACTAA	ACCACTTAAA	AGAAAACCTG	600
AAAATTATTC	ACAGAGATAT	CAAACCTTCC	AATATTCTTC	TGGACAGAAG	TGGAAATATT	660
AAGCTCTGTG	ACTTCGGCAT	CAGTGGACAG	CTTGTGGACT	CTATTGCCAA	GACAAGAGAT	720
GCTGGCTGTA	GGCCATACAT	GGCACCTGAA	AGAATAGACC	CAAGCGCATC	ACGACAAGGA	780
TATGATGTCC	GCTCTGATGT	CTGGAGTTTG	GGGATCACAT	TGTATGAGTT	GGCCACAGGC	840
CGATTTCCCT	ATCCAAAGTG	GAATAGTGTA	TTTGATCAAC	TAACACAAGT	CGTGAAAGGA	900
GATCCTCCGC	AGCTGAGTAA	TTCTGAGGAA	AGGGAATTCT	CCCCGAGTTT	CATCAACTTT	960
GTCAACTTGT	GCCTTACGAA	GGATGAATCC	AAAAGGCCAA	AGTATAAAGA	GCTTCTGAAA	1020
CATCCCTTTA	TTTTGATGTA	TGAAGAACGT	GCCGTTGAGG	TCGCATGCTA	TGTTTGTAAA	1080

ATCCTGGATC	AAATGCCAGC	TACTCCCAGC	TCTCCCATGT	ATGTCGATTG	ATATCGYTGC	1140
TACATCAGAC	TCTAGAAAAA	AGGGCTGAGA	GGAAGCAAGA	CGTAAAGAAT	TTTCATCCCG	1200
TATCACAGTG	TTTTTATTGC	TCGCCCAGAC	ACCATGTGCA	ATAAGATTGG	TGTTCGTTTC	1260
CATCATGTCT	GTATACTCCT	GTCACCTAGA	ACGTGCATCC	TTGTAATACC	TGATTGATCA	1320
CACAGTGTTA	GTGCTGGTCA	GAGAGACCTC	ATCCTGCTCT	TTTGTGATGA	ACATATTCAT	1380
GAAATGTGGA	AGTCAGTACG	ATCAAGTTGT	TGACTGTGAT	TAGATCACAT	CTTAAATTCA	1440
TTTCTAGACT	CAAAACCTGG	AGATGCAGCT	ACTGGAATGG	TGTTTTGTCA	GACTTCCAAA	1500
TCCTGGAAGG	ACACAGTGAT	GAATGTACTA	TATCTGAACA	TAGAAACTCG	GGCTTGAGTG	1560
AGAAGAGCTT	GCACAGCCAA	CGAGACACAT	TGCCTTCTGG	AGCTGGGAGA	CAAAGGAGGA	1620
ATTTACTTTC	TTCACCAAGT	GCAATAGATT	ACTGATGTGA	TATTCTGTTG	CTTTACAGTT	1680
ACAGTTGATG	TTTGGGGATC	GATGTGCTCA	GCCAAATTTT	CTGTTTGAAA	TATCATGTTA	1740
AATTAGAATG	AATTTATCTT	TACCAAAAAC	CATGTTGCGT	TCAAAGAGGT	GAACATTAAA	1800
ATATAGAGAC	AGGACAGAAT	GTGTTCTTTT	CTCCTCTACC	AGTCCTATTT	TTCAATGGGA	1860
AGACTCAGGA	GTCTGCCACT	TGTCAAAGAA	GGTGCTGATC	CTAAGAATTT	TTCAATCTCA	1920
GAATTCGGTG	TGCTGCCAAC	TTGATGTTCC	ACCTGCCACA	AACCACCAGG	ACTGAAAGAA	1980
GAAAACAGTA	CAGAAGGCAA	AGTTTACAGA	TGTTTTTAAT	TCTAGTATTT	TATCTGGAAC	2040
AAC TTGTAGC	AGCTATATAT	TTCCCCTTGG	TCCCAAGCCT	GATACTTTAG	CCATCATAAC	2100
TGACTAACAG	GGAGAAGTAG	CTAGTAGCAA	TGTGCCTTGA	TTGATTAGAT	AAAGATTCTT	2160
AGTAGGCAGC	AAAAGACCAA	ATCTCAGTTG	TTTGCTTCTT	GCCATCACTG	GTCCAGGTCT	2220
TCAGTTTCCG	AATCTCTTTC	CCTTCCCCTG	TGGTCTATTG	TCGCTATGTG	ACTTGCGCTT	2280
AATCCAATAT	TTTGCCCTTTT	TTCTATATCA	AAAAACCTTT	ACAGTTAGCA	GGGATGTTCC	2340
TTACCCGAGGA	TTTTTAACCC	CCAATCTCTC	ATAATCGCTA	GTGTTTAAAA	GGCTAAGAAT	2400
AGTGGGGCCC	AACCGATGTG	GTAGGTGATA	AAGAGGCATC	TTTTCTAGAG	ACACATTGGA	2460
GCAGATGAGG	ATCCGAAACG	GCAGCCTTTA	CGTTCATCAC	CTGCTAGAAC	CTCTCGTAGT	2520
CCATCACCAT	TTCTTGGCAT	TGGAATTCTA	CTGGAAAAAA	ATACAAAAAG	CAAAACAAAA	2580
CCCTCAGCAC	TGTTACAAGA	GGCCATTTAA	GTATCTTG TG	CTTCTTCACT	TACCCATTAG	2640
CCAGGTTCTC	ATTAGGTTTT	GCTTGGGCCT	CCCTGGCACT	GAACCTTAGG	CTTTGTATGA	2700
CAGTGAAGCA	GCACTGTGAG	TGGTTCAAGC	ACACTGGAAT	ATAAAACAGT	CATGGCCTGA	2760
GATGCAGGTG	ATGCCATTAC	AGAACCAAAT	CGTGGCACGT	ATTGCTGTGT	CTCCTCTCAG	2820
AGTGACAGTC	ATAAATACTG	TCAAACAATA	AAGGGAGAAT	GGTGCTGTTT	AAAGTCACAT	2880
CCCTGTAAAT	TGCAGAATTC	AAAAGTGATT	ATCTCTTTGA	TCTACTTGCC	TCATTTCCCT	2940
ATCTTCTCCC	CCACGGTATC	CTAAACTTTA	GACTTCCCAC	TGTTCTGAAA	GGAGACATTG	3000
CTCTATGTCT	GCCTTCGACC	ACAGCAAGCC	ATCATCCTCC	ATTGCTCCCG	GGGACTCAAG	3060
AGGAATCTGT	TTCTCTGCTG	TCAACTTCCC	ATCTGGCTCA	GCATAGGGTC	ACTTTGCCAT	3120
TATGCAAATG	GAGATAAAAG	CAATTCTGGC	TGTCCAGGAT	CTAATCTGAC	CGTTCATTAT	3180
TGTGGATGAC	CACATAAGAA	GGCAATTTTA	GTGTATTAAAT	CATAGATTAT	TATAAACTAT	3240
AAACTTAAGG	GCAAGGAGTT	TATTACAATG	TATCTTTATT	AAAACAAAAG	GGTGTATAGT	3300
GTTCACAAAC	TGTGAAAATA	GTGTAAGAAC	TGTACATTGT	GAGCTCTGGT	TATTTTTCTC	3360
TTGTACCATA	GAAAAATGTA	TAAAAATTAT	CAAAAAGCTA	ATGTGCAGGG	ATATTGCCTT	3420
ATTTGTCTGT	AAAAAATGGA	GCTCAGTAAC	ATAACTGCTT	CTTGAGCTT	TGGAATATTT	3480
TATCCTGTAT	TCTTGTTT					3498

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: peptide
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

				5				10						15			
Met	Gln	Gly	Lys	Arg	Lys	Ala	Leu	Lys	Leu	Asn	Phe	Ala	Asn	Pro	Pro		
			20					25					30				
Phe	Lys	Ser	Thr	Ala	Arg	Phe	Thr	Leu	Asn	Pro	Asn	Pro	Thr	Gly	Val		
		35					40					45					
Gln	Asn	Pro	His	Ile	Glu	Arg	Leu	Arg	Thr	His	Ser	Ile	Glu	Ser	Ser		
	50					55					60						
Gly	Lys	Leu	Lys	Ile	Ser	Pro	Glu	Gln	His	Trp	Asp	Phe	Thr	Ala	Glu		
65					70					75					80		
Asp	Leu	Lys	Asp	Leu	Gly	Glu	Ile	Gly	Arg	Gly	Ala	Tyr	Gly	Ser	Val		
				85				90						95			
Asn	Lys	Met	Val	His	Lys	Pro	Ser	Gly	Gln	Ile	Met	Ala	Val	Lys	Arg		
			100					105					110				
Ile	Arg	Ser	Thr	Val	Asp	Glu	Lys	Glu	Gln	Lys	Gln	Leu	Leu	Met	Asp		
		115					120					125					
Leu	Asp	Val	Val	Met	Arg	Ser	Ser	Asp	Cys	Pro	Tyr	Ile	Val	Gln	Phe		
	130					135					140						
Tyr	Gly	Ala	Leu	Phe	Arg	Glu	Gly	Asp	Cys	Trp	Ile	Cys	Met	Glu	Leu		
145					150					155				160			
Met	Ser	Thr	Ser	Phe	Asp	Lys	Phe	Tyr	Lys	Tyr	Val	Tyr	Ser	Val	Leu		
				165				170						175			
Asp	Asp	Val	Ile	Pro	Glu	Glu	Ile	Leu	Gly	Lys	Ile	Thr	Leu	Ala	Thr		
			180					185					190				
Val	Lys	Ala	Leu	Asn	His	Leu	Lys	Glu	Asn	Leu	Lys	Ile	Ile	His	Arg		
		195					200					205					
Asp	Ile	Lys	Pro	Ser	Asn	Ile	Leu	Leu	Asp	Arg	Ser	Gly	Asn	Ile	Lys		
	210				215						220						
Leu	Cys	Asp	Phe	Gly	Ile	Ser	Gly	Gln	Leu	Val	Asp	Ser	Ile	Ala	Lys		
225					230					235				240			
Thr	Arg	Asp	Ala	Gly	Cys	Arg	Pro	Tyr	Met	Ala	Pro	Glu	Arg	Ile	Asp		
			245					250					255				
Pro	Ser	Ala	Ser	Arg	Gln	Gly	Tyr	Asp	Val	Arg	Ser	Asp	Val	Trp	Ser		
		260						265					270				
Leu	Gly	Ile	Thr	Leu	Tyr	Glu	Leu	Ala	Thr	Gly	Arg	Phe	Pro	Tyr	Pro		
		275					280					285					
Lys	Trp	Asn	Ser	Val	Phe	Asp	Gln	Leu	Thr	Gln	Val	Val	Lys	Gly	Asp		
	290					295					300						
Pro	Pro	Gln	Leu	Ser	Asn	Ser	Glu	Glu	Arg	Glu	Phe	Ser	Pro	Ser	Phe		
305					310					315					320		
Ile	Asn	Phe	Val	Asn	Leu	Cys	Leu	Thr	Lys	Asp	Glu	Ser	Lys	Arg	Pro		
				325					330					335			
Lys	Tyr	Lys	Glu	Leu	Leu	Lys	His	Pro	Phe	Ile	Leu	Met	Tyr	Glu	Glu		
			340					345					350				
Arg	Ala	Val	Glu	Val	Ala	Cys	Tyr	Val	Cys	Lys	Ile	Leu	Asp	Gln	Met		
		355					360			363							
Pro	Ala	Thr	Pro	Ser	Ser	Pro	Met	Tyr	Val	Asp							

(2) INFORMATION FOR SEQ ID NO:7:  
 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3554 base pairs  
 (B) TYPE: nucléic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAACAATGGC	GGCTCCGAGC	CCGAGCGGTG	GCGGCGGCAG	CGGCACCCCC	GGCCCCGTAG	60
GGTCCCCGGC	GCCAGGCCAC	CCGGCCGTCA	GCAGCATGCA	GGGTAAACGC	AAAGCACTGA	120
AGTTGAATTT	TGCAAATCCA	CCTTTCAAAT	CTACAGCAAG	GTTTACTCTG	AATCCCAATC	180
CTACAGGAGT	TCAAAACCCA	CACATAGAGA	GA CTGAGAAC	ACACAGCATT	GAGTCATCAG	240
GAAAACTGAA	GATCTCCCCCT	GAACAACACT	GGGATTTTAC	TGCAGAGGAC	TTGAAAGACC	300
TTGGAGAAAT	TGGACGAGGA	GCTTATGGTT	CTGTCAACAA	AATGGTCCAC	AAACCAAGTG	360
GGCAAATAAT	GGCAGTTAAA	AGAATTCGGT	CAACAGTGGA	TGAAAAAGAA	CAAAAACAAC	420
TTCTTATGGA	TTTGGATGTA	GTAATGCGGA	GTAGTGATTG	CCCATACATT	GTTCAGTTTT	480
ATGGTGCAC	CTTCAGAGAG	GGTGACTGTT	GGATCTGTAT	GGAACCTCATG	TCTACCTCGT	540
TTGATAAGTT	TTACAAATAT	GTATATAGTG	TATTAGATGA	TGTTATTCCA	GAAGAAATTT	600
TAGGCAAAAT	CACTTTAGCA	ACTGTGAAAG	CACTAAACCA	CTTAAAAGAA	AACTTGAAAA	660
TTATTCACAG	AGATATCAAA	CCTTCCAATA	TTCTTCTGGA	CAGAAGTGGA	AATATTAAGC	720
TCTGTGACTT	CGGCATCAGT	GGACAGCTTG	TGGACTCTAT	TGCCAAGACA	AGAGATGCTG	780
GCTGTAGGCC	ATACATGGCA	CCTGAAAGAA	TAGACCCAAG	CGCATCACGA	CAAGGATATG	840
ATGTCCGCTC	TGATGTCTGG	AGTTTGGGGA	TCACATTGTA	TGAGTTGGCC	ACAGGCCGAT	900
TTCCCTTATCC	AAAGTGGAAT	AGTGTATTTG	ATCAACTAAC	ACAAGTCGTG	AAAGGAGATC	960
CTCCGCAGCT	GAGTAATTCT	GAGGAAAGGG	AATTCTCCCC	GAGTTTTCATC	AACTTTGTCA	1020
ACTTGTGCCT	TACGAAGGAT	GAATCCAAAA	GGCCAAAGTA	TAAAGAGCTT	CTGAAACATC	1080
CTTTTATTTT	GATGTATGAA	GAACGTGCCG	TTGAGGTCGC	ATGCTATGTT	TGTAAAATCC	1140
TGGATCAAAT	GCCAGCTACT	CCCAGCTCTC	CCATGTATGT	CGATTGATAT	CGYTGTCTACA	1200
TCAGACTCTA	GAAAAAAGGG	CTGAGAGGAA	GCAAGACGTA	AAGAATTTTC	ATCCCGTATC	1260
ACAGTGTTTT	TATTGCTCGC	CCAGACACCA	TGTGCAATAA	GATTGGTGTT	CGTTTCCATC	1320
ATGTCTGTAT	ACTCCTGTCA	CCTAGAACGT	GCATCCTTGT	AATACCTGAT	TGATCACACA	1380
GTGTTAGTGC	TGGTCAGAGA	GACCTCATCC	TGCTCTTTTG	TGATGAACAT	ATTCATGAAA	1440
TGTGGAAGTC	AGTACGATCA	AGTTGTTGAC	TGTGATTAGA	TCACATCTTA	AATTCATTTT	1500
TAGACTCAAA	ACCTGGAGAT	GCAGCTACTG	GAATGGTGTT	TTGTCAGACT	TCCAAATCCT	1560
GGAAGGACAC	AGTGATGAAT	GTACTATATC	TGAACATAGA	AACTCGGGCT	TGAGTGAGAA	1620
GAGCTTGCAC	AGCCAACGAG	ACACATTGCC	TTCTGGAGCT	GGGAGACAAA	GGAGGAATTT	1680
ACTTTCCTCA	CCAAGTGCAA	TAGATTACTG	ATGTGATATT	CTGTTGCTTT	ACAGTTACAG	1740
TTGATGTTTT	GGGATCGATG	TGCTCAGCCA	AATTTCTGT	TTGAAATATC	ATGTTAAATT	1800
AGAAATGAATT	TATCTTTTACC	AAAAACCATG	TTGCGTTCAA	AGAGGTGAAC	ATTAAAATAT	1860
AGAGACAGGA	CAGAATGTGT	TCTTTTCTCC	TCTACCAGTC	CTATTTTTTCA	ATGGGAAGAC	1920
TCAGGAGTCT	GCCACTTGTC	AAAGAAGGTG	CTGATCCTAA	GAATTTTTTCA	TTCTCAGAAT	1980
TCGGTGTGCT	GCCAACTTGA	TGTTCCACCT	GCCACAAACC	ACCAGGACTG	AAAGAAGAAA	2040
ACAGTACAGA	AGGCAAAGTT	TACAGATGTT	TTTAATTCTA	GTATTTTATC	TGGAACAACT	2100
TGTAGCAGCT	ATATATTTCC	CCTTGGTCCC	AAGCCTGATA	CTTTAGCCAT	CATAACTCAC	2160
TAACAGGGAG	AAGTAGCTAG	TAGCAATGTG	CCTTGATTGA	TTAGATAAAG	ATTTCTAGTA	2220
GGCAGCAAAA	GACCAAATCT	CAGTTGTTTG	CTTCTTGCCA	TCAGTGGTCC	AGGTCTTCAG	2280
TTTCCGAATC	TCTTTCCCTT	CCCCTGTGGT	CTATTGTCGC	TATGTGACTT	GCGCTTAATC	2340
CAATATTTTG	CCTTTTTTCT	ATATCAAAAA	ACCTTTACAG	TTAGCAGGGA	TGTTCTTTAC	2400
CGAGGATTTT	TAACCCCCAA	TCTCTCATAA	TCGCTAGTGT	TTAAAAGGCT	AAGAATAGTG	2460
GGGCCCAACC	GATGTGGTAG	GTGATAAAGA	GGCATCTTTT	CTAGAGACAC	ATTGGACCAG	2520
ATGAGGATCC	GAAACGGCAG	CCTTTACGTT	CATCACCTGC	TAGAACCTCT	CGTAGTCCAT	2580



CACCATTCT TGGCATTGGA ATTCTACTGG AAAAAAATAC AAAAAGCAAA ACAAACCCT 2640  
 CAGCACTGTT ACAAGAGGCC ATTTAAGTAT CTTGTGCTTC TTCACTTACC CATTAGCCAG 2700  
 GTTCTCATTA GGTTTTGCTT GGGCCTCCCT GGCAGTGAAC CTTAGGCTTT GTATGACAGT 2760  
 GAAGCAGCAC TGTGAGTGGT TCAAGCACAC TGGAATATAA AACAGTCATG GCCTGAGATG 2820  
 CAGGTGATGC CATTACAGAA CCAATCGTG GCACGTATTG CTGTGTCTCC TCTCAGAGTG 2880  
 ACAGTCATAA ATACTGTCAA ACAATAAAGG GAGAATGGTG CTGTTTAAAG TCACATCCCT 2940  
 GTAAATTGCA GAATTCAAAA GTGATTATCT CTTTGATCTA CTTGCCTCAT TTCCTATCT 3000  
 TCTCCCCCAC GGTATCCTAA ACTTTAGACT TCCCAGTGT CTGAAAGGAG ACATTGCTCT 3060  
 ATGTCTGCCT TCGACCACAG CAAGCCATCA TCCTCCATTG CTCCCGGGA CTCAAGAGGA 3120  
 ATCTGTTTCT CTGCTGTCAA CTTCCCATCT GGCTCAGCAT AGGGTCACTT TGCCATTATG 3180  
 CAAATGGAGA TAAAAGCAAT TCTGGCTGTC CAGGAGCTAA TCTGACCGTT CTATTGTGTG 3240  
 GATGACCACA TAAGAAGGCA ATTTAGTGT ATTAATCATA GATTATTATA AACTATAAAC 3300  
 TTAAGGGCAA GGAGTTTATT ACAATGTATC TTTATTAAAA CAAAAGGGTG TATAGTGTTT 3360  
 ACAAACTGTG AAAATAGTGT AAGAACTGTA CATTGTGAGC TCTGGTTATT TTTCTCTTGT 3420  
 ACCATAGAAA AATGTATAAA AATTATCAA AAGCTAATGT GCAGGGATAT TGCCTTATTT 3480  
 GTCTGTAAAA AATGGAGCTC AGTAACATAA CTGCTTCTTG GAGCTTTGGA ATATTTTATC 3540  
 CTGTATTCTT GTTT 3554

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 404 amino acids

(B) TYPE: peptide

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ala	Ala	Pro	Ser	Pro	Ser	Gly	Gly	Gly	Ser	Gly	Thr	Pro	Gly
			20				25					30		
Pro	Val	Gly	Ser	Pro	Ala	Pro	Gly	His	Pro	Ala	Val	Ser	Ser	Met
		35					40				45			Gln
Gly	Lys	Arg	Lys	Ala	Leu	Lys	Leu	Asn	Phe	Ala	Asn	Pro	Pro	Phe
	50					55				60				Lys
Ser	Thr	Ala	Arg	Phe	Thr	Leu	Asn	Pro	Asn	Pro	Thr	Gly	Val	Gln
	65				70					75				80
Pro	His	Ile	Glu	Arg	Leu	Arg	Thr	His	Ser	Ile	Glu	Ser	Ser	Gly
			85					90					95	Lys
Leu	Lys	Ile	Ser	Pro	Glu	Gln	His	Trp	Asp	Phe	Thr	Ala	Glu	Asp
			100					105					110	Leu
Lys	Asp	Leu	Gly	Glu	Ile	Gly	Arg	Gly	Ala	Tyr	Gly	Ser	Val	Asn
	115					120					125			Lys
Met	Val	His	Lys	Pro	Ser	Gly	Gln	Ile	Met	Ala	Val	Lys	Arg	Ile
	130					135					140			Arg
Ser	Thr	Val	Asp	Glu	Lys	Glu	Gln	Lys	Gln	Leu	Leu	Met	Asp	Leu
	145				150					155				160
Val	Val	Met	Arg	Ser	Ser	Asp	Cys	Pro	Tyr	Ile	Val	Gln	Phe	Tyr
			165						170					Gly
Ala	Leu	Phe	Arg	Glu	Gly	Asp	Cys	Trp	Ile	Cys	Met	Glu	Leu	Met
			180					185					190	Ser
Thr	Ser	Phe	Asp	Lys	Phe	Tyr	Lys	Tyr	Val	Tyr	Ser	Val	Leu	Asp
														Asp

Val	Ile	195	Pro	Glu	Glu	Ile	Leu	200	Gly	Lys	Ile	Thr	Leu	205	Ala	Thr	Val	Lys
	210						215						220					
Ala	Leu	Met	His	Leu	Lys	Glu	Asn	Leu	Lys	Ile	Ile	His	Arg	Asp	Ile			
225					230					235					240			
Lys	Pro	Ser	Asn	Ile	Leu	Leu	Asp	Arg	Ser	Gly	Met	Ile	Lys	Leu	Cys			
			245						250					255				
Asp	Phe	Gly	Ile	Ser	Gly	Gln	Leu	Val	Asp	Ser	Ile	Ala	Lys	Thr	Arg			
		260						265					270					
Asp	Ala	Gly	Cys	Arg	Pro	Tyr	Met	Ala	Pro	Glu	Arg	Ile	Asp	Phe	Ser			
		275					280						285					
Ala	Ser	Arg	Gln	Gly	Tyr	Asp	Val	Arg	Ser	Asp	Val	Trp	Ser	Leu	Gly			
	290					295					300							
Ile	Thr	Leu	Tyr	Glu	Leu	Ala	Thr	Gly	Arg	Phe	Pro	Tyr	Pro	Lys	Trp			
305					310					315					320			
Asn	Ser	Val	Phe	Asp	Gln	Leu	Thr	Gln	Val	Lys	Gly	Asp	Pro	Pro				
			325						330				335					
Gln	Leu	Ser	Asn	Ser	Glu	Glu	Arg	Glu	Phe	Ser	Pro	Ser	Phe	Ile	Asn			
		340						345					350					
Phe	Val	Asn	Leu	Cys	Leu	Thr	Lys	Asp	Glu	Ser	Lys	Arg	Pro	Lys	Tyr			
		355					360					365						
Lys	Glu	Leu	Leu	Lys	His	Pro	Phe	Ile	Leu	Met	Tyr	Glu	Glu	Arg	Ala			
	370					375					380							
Val	Glu	Val	Ala	Cys	Tyr	Val	Cys	Lys	Ile	Leu	Asp	Gln	Met	Pro	Ala			
385					390			393										
Thr	Pro	Ser	Ser	Pro	Met	Tyr	Val	Asp										

(2) INFORMATION FOR SEQ ID NO:9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTCCCAACAA	TGGCGGCTCC	GAGCCCGAGC	GGCGGCGGCG	GCTCCGGGGG	CGGCAGCGGC	60
AGCGGCACCC	CCGGCCCCGT	AGGGTCCCCG	GCGCCAGGCC	ACCCGGCCGT	CAGCAGCATG	120
CAGGGTAAAC	GCAAAGCACT	GAAGTTGAAT	TTTGCAAATC	CACCTTTCAA	ATCTACAGCA	180
AGGTTTACTC	TGAATCCCAA	TCCTACAGGA	GTTCAAAACC	CACACATAGA	GAGACTGAGA	240
ACACACAGCA	TTGAGTCATC	AGGAAACTG	AAGATCTCCC	CTGAACAACA	CTGGGATTTT	300
ACTGCAGAGG	ACTTGAAAGA	CCTTGAGAG	ATTGGACGAG	GAGCTTATGG	TTCTGTCAAC	360
AAAATGGTCC	ACAAACCAAG	TGGGCAAATA	ATGGCAGTTA	AAAGAATTCT	GTCAACAGTG	420
GATGAAAAAG	AACAAAAACA	ACTTCTTATG	GATTTGGATG	TAGTAATGCG	GAGTAGTGAT	480
TGCCCATACA	TTGTTTCAGT	TTATGGTGCA	CTCTTCAGAG	AGGGTGACTG	TTGGATCTGT	540
ATGGAACCTCA	TGTCTACCTC	GTTTGATAAG	TTTTACAAAT	ATGTATATAG	TGTATTAGAT	600
GATGTTATTC	CAGAAGAAAT	TTTAGGCAAA	ATCACTTTAG	CAACTGTGAA	AGCACTAAAC	660
CACTTAAAG	AAAACCTTGA	AATTATTCAC	AGAGATATCA	AACCTTCCAA	TATTCTTCTG	720
GACAGAAGTG	GAAATATTAA	GCTCTGTGAC	TTCGGCATCA	GTGGACAGCT	TGTGGACTCT	780
ATTGCCAAGA	CAAGAGATGC	TGGCTGTAGG	CCATACATGG	CACCTGAAAG	AATAGACCCA	840

AGCGCATCAC	GACAAGGATA	TGATGTCCGC	TCTGATGTCT	GGAGTTTGGG	GATCACATTG	900
TATGAGTTGG	CCACAGGCCG	ATTTCCCTTAT	CCAAAGTGGA	ATAGTGTATT	TGATCAACTA	960
ACACAAGTCG	TGAAAGGAGA	TCCTCCGCAG	CTGAGTAATT	CTGAGGAAAG	GGAATTCTCC	1020
CCGAGTTTCA	TCAACTTTGT	CAACTTGTGC	CTTACGAAGG	ATGAATCCAA	AAGGCCAAAG	1080
TATAAAGAGC	TTCTGAAACA	TCCCTTTATT	TTGATGTATG	AAGAACGTGC	CGTTGAGGTC	1140
GCATGCTATG	TTTGTA AAAAT	CCTGGATCAA	ATGCCAGCTA	CTCCCAGCTC	TCCCATGTAT	1200
GTGCGATTGAT	ATCGCTGCTA	CATCAGACTC	TAGAAAAAAG	GGCTGAGAGG	AAGCAAGACG	1260
TAAAGAATTT	TCATCCCGTA	TCACAGTGTT	TTTATTGCTC	GCCCAGACAC	CATGTGCAAT	1320
AAGATTGGTG	TTGCTTTCCA	TCATGTCTGT	ATACTCCTGT	CACCTAGAAC	GTGCATCCTT	1380
GTAATACCTG	ATTGATCACA	CAGTGTTAGT	GCTGGTCAGA	GAGACCTCAT	CCTGCTCTTT	1440
TGTGATGAAC	ATATTCATGA	AATGTGGAAG	TCAGTACGAT	CAAGTTGTTG	ACTGTGATTA	1500
GATCACATCT	TAAATTCATT	TCTAGACTCA	AAACCTGGAG	ATGCAGCTAC	TGGAATGGTG	1560
TTTTGTGAGA	CTTCCAAATC	CTGGAAGGAC	ACAGTGATGA	ATGTACTATA	TCTGAACATA	1620
GAAACTCGGG	CTTGAGTGAG	AAGAGCTTGC	ACAGCCAACG	AGACACATTG	CCTTCTGGAG	1680
CTGGGAGACA	AAGGAGGAAT	TTACTTTCTT	CACCAAGTGC	AATAGATTAC	TGATGTGATA	1740
TTCTGTTGCT	TTACAGTTAC	AGTTGATGTT	TGGGGATCGA	TGTGCTCAGC	CAAATTTCTT	1800
GTTTGAAATA	TCATGTTAAA	TTAGAATGAA	TTTATCTTTA	CCAAAAACCA	TGTTGCGTTC	1860
AAAGAGGTGA	ACATTAAAAAT	ATAGAGACAG	GACAGAATGT	GTTCTTTTCT	CCTCTACCAG	1920
TCCTATTTTT	CAATGGGAAG	ACTCAGGAGT	CTGCCACTTG	TCAAAGAAGG	TGCTGATCCT	1980
AAGAATTTTT	CATTCTCAGA	ATTCGGTGTG	CTGCCAACTT	GATGTTCCAC	CTGCCACAAA	2040
CCACCAGGAC	TGAAAGAAGA	AAACAGTACA	GAAGGCAAAG	TTTACAGATG	TTTTTAATTC	2100
TAGTATTTTA	TCTGGAACAA	CTTGTTAGCAG	CTATATATTT	CCCCTTGTC	CCAAGCCTGA	2160
TACTTTAGCC	ATCATAACTC	ACTAACAGGG	AGAAGTAGCT	AGTAGCAATG	TGCCCTTGATT	2220
GATTAGATAA	AGATTTCTAG	TAGGCAGCAA	AAGACCAAAT	CTCAGTTGTT	TGCTTCTTGC	2280
CATCACTGGT	CCAGGTCTTC	AGTTTCCGAA	TCTCTTTCCC	TTCCCCTGTG	GTCTATTGTC	2340
GCTATGTGAC	TTGCGCTTAA	TCCAATATTT	TGCCTTTTTT	CTATATCAAA	AAACCTTTAC	2400
AGTTAGCAGG	GATGTTCTTT	ACCGAGGATT	TTTAACCCCC	AATCTCTCAT	AATCGCTAGT	2460
GTTTAAAAGG	CTAAGAATAG	TGGGGCCCAA	CCGATGTGGT	AGGTGATAAA	GAGGCATCTT	2520
TTCTAGAGAC	ACATTGGACC	AGATGAGGAT	CCGAAACGGC	AGCCTTTACG	TTCATCACCT	2580
GCTAGAACCT	CTCGTAGTCC	ATCACCATTT	CTTGGCATTG	GAATTCTACT	GGAAAAAAT	2640
ACAAAAAGCA	AAACAAAACC	CTCAGCACTG	TTACAAGAGG	CCATTTAAGT	ATCTTGTGCT	2700
TCTTCACTTA	CCCATTAGCC	AGGTTCTCAT	TAGGTTTTCG	TTGGGCTTCC	CTGGCACTGA	2760
ACCTTAGGCT	TTGTATGACA	GTGAAGCAGC	ACTGTGAGTG	GTTCAAGCAC	ACTGGAATAT	2820
AAAACAGTCA	TGGCCTGAGA	TGCAGGTGAT	GCCATTACAG	AACCAAATCG	TGGCACGTAT	2880
TGCTGTGTCT	CCTCTCAGAG	TGACAGTCAT	AAATACTGTC	AAACAATAAA	GGGAGAATGG	2940
TGCTGTTTAA	AGTCACATCC	CTGTAAATTG	CAGAATTCAA	AAGTGATTAT	CTCTTTGATC	3000
TACTTGCCCTC	ATTTCCCTAT	CTTCTCCCCC	ACGGTATCCT	AAACTTTAGA	CTTCCCCTG	3060
TTCTGAAAGG	AGACATTGCT	CTATGTCTGC	CTTCGACCAC	AGCAAGCCAT	CATCCTCCAT	3120
TGCTCCCGGG	GACTCAAGAG	GAATCTGTTT	CTCTGCTGTC	AACCTCCCAT	CTGGCTCAGC	3180
ATAGGGTCAC	TTTGCCATTA	TGCAAAATGGA	GATAAAAGCA	ATTCTGGCTG	TCCAGGAGCT	3240
AATCTGACCG	TTCTATTGTG	TGGATGACCA	CATAAGAAGG	CAATTTTAGT	GTATTAATCA	3300
TAGATTATTA	TAAACTATAA	ACTTAAGGGC	AAGGAGTTTA	TTACAATGTA	TCTTTATTAA	3360
AACAAAAGGG	TGTATAGTGT	TCACAAACTG	TGAAAATAGT	GTAAGAAGCT	TACATTGTGA	3420
GCTCTGGTTA	TTTTTCTCTT	GTACCATAGA	AAAATGTATA	AAAATTATCA	AAAAGCTAAT	3480
GTGCAGGGAT	ATTGCCTTAT	TTGTCTGTAA	AAAATGGAGC	TCAGTAACAT	AACTGCTTCT	3540
TGGAGCTTTG	GAATATTTTA	TCCTGTATTC	TTGTTT			3600
						3636

(2) INFORMATION FOR SEQ ID NO:10:  
 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids

(B) TYPE: peptide

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

				5					10					15		
Met	Ala	Ala	Pro	Ser	Pro	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	
			20					25					30			
Gly	Ser	Gly	Thr	Pro	Gly	Pro	Val	Gly	Ser	Pro	Ala	Pro	Gly	His	Pro	
		35					40					45				
Ala	Val	Ser	Ser	Met	Gln	Gly	Lys	Arg	Lys	Ala	Leu	Lys	Leu	Asn	Phe	
	50					55					60					
Ala	Asn	Pro	Pro	Phe	Lys	Ser	Thr	Ala	Arg	Phe	Thr	Leu	Asn	Pro	Asn	
65					70				75					80		
Pro	Thr	Gly	Val	Gln	Asn	Pro	His	Ile	Glu	Arg	Leu	Arg	Thr	His	Ser	
			85						90					95		
Ile	Glu	Ser	Ser	Gly	Lys	Leu	Lys	Ile	Ser	Pro	Glu	Gln	His	Trp	Asp	
			100					105					110			
Phe	Thr	Ala	Glu	Asp	Leu	Lys	Asp	Leu	Gly	Glu	Ile	Gly	Arg	Gly	Ala	
		115					120					125				
Tyr	Gly	Ser	Val	Asn	Lys	Met	Val	His	Lys	Pro	Ser	Gly	Gln	Ile	Met	
	130					135					140					
Ala	Val	Lys	Arg	Ile	Arg	Ser	Thr	Val	Asp	Glu	Lys	Glu	Gln	Lys	Gln	
145					150				155					160		
Leu	Leu	Met	Asp	Leu	Asp	Val	Val	Met	Arg	Ser	Ser	Asp	Cys	Pro	Tyr	
			165						170					175		
Ile	Val	Gln	Phe	Tyr	Gly	Ala	Leu	Phe	Arg	Glu	Gly	Asp	Cys	Trp	Ile	
		180						185					190			
Cys	Met	Glu	Leu	Met	Ser	Thr	Ser	Phe	Asp	Lys	Phe	Tyr	Lys	Tyr	Val	
	195						200					205				
Tyr	Ser	Val	Leu	Asp	Asp	Val	Ile	Pro	Glu	Glu	Ile	Leu	Gly	Lys	Ile	
	210					215					220					
Thr	Leu	Ala	Thr	Val	Lys	Ala	Leu	Asn	His	Leu	Lys	Glu	Asn	Leu	Lys	
225					230				235					240		
Ile	Ile	His	Arg	Asp	Ile	Lys	Pro	Ser	Asn	Ile	Leu	Leu	Asp	Arg	Ser	
			245						250					255		
Gly	Asn	Ile	Lys	Leu	Cys	Asp	Phe	Gly	Ile	Ser	Gly	Gln	Leu	Val	Asp	
		260						265					270			
Ser	Ile	Ala	Lys	Thr	Arg	Asp	Ala	Gly	Cys	Arg	Pro	Tyr	Met	Ala	Pro	
	275						280					285				
Glu	Arg	Ile	Asp	Pro	Ser	Ala	Ser	Arg	Gln	Gly	Tyr	Asp	Val	Arg	Ser	
	290					295					300					
Asp	Val	Trp	Ser	Leu	Gly	Ile	Thr	Leu	Tyr	Glu	Leu	Ala	Thr	Gly	Arg	
305					310				315					320		
Phe	Pro	Tyr	Pro	Lys	Trp	Asn	Ser	Val	Phe	Asp	Gln	Leu	Thr	Gln	Val	
			325						330					335		
Val	Lys	Gly	Asp	Pro	Pro	Gln	Leu	Ser	Asn	Ser	Glu	Glu	Arg	Glu	Phe	
		340					345						350			
Ser	Pro	Ser	Phe	Ile	Asn	Phe	Val	Asn	Leu	Cys	Leu	Thr	Lys	Asp	Glu	

	355		360		365										
Ser	Lys	Arg	Pro	Lys	Tyr	Lys	Glu	Leu	Leu	Lys	His	Pro	Phe	Ile	Leu
	370					375					380				
Met	Tyr	Glu	Glu	Arg	Ala	Val	Glu	Val	Ala	Cys	Tyr	Val	Cys	Lys	Ile
385					390					395				399	
Leu	Asp	Gln	Met	Pro	Ala	Thr	Pro	Ser	Ser	Pro	Met	Tyr	Val	Asp	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 amino acids

(B) TYPE: peptide

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

		5					10						15		
Met	Pro	Lys	Lys	Lys	Pro	Thr	Pro	Ile	Gln	Leu	Asn	Pro	Ala	Pro	Asp
		20					25						30		
Gly	Ser	Ala	Val	Asn	Gly	Thr	Ser	Ser	Ala	Glu	Thr	Asn	Leu	Glu	Ala
		35					40					45			
Leu	Gln	Lys	Lys	Leu	Glu	Glu	Leu	Glu	Leu	Asp	Glu	Gln	Gln	Arg	Lys
		50				55					60				
Arg	Leu	Glu	Ala	Phe	Leu	Thr	Gln	Lys	Gln	Lys	Val	Gly	Glu	Leu	Lys
65					70					75				80	
Asp	Asp	Asp	Phe	Glu	Lys	Ile	Ser	Glu	Leu	Gly	Ala	Gly	Asn	Gly	Gly
		85					90						95		
Val	Val	Phe	Lys	Val	Ser	His	Lys	Pro	Ser	Gly	Leu	Val	Met	Ala	Arg
		100					105						110		
Lys	Leu	Ile	His	Leu	Glu	Ile	Lys	Pro	Ala	Ile	Arg	Asn	Gln	Ile	Ile
		115					120					125			
Arg	Glu	Leu	Gln	Val	Leu	His	Glu	Cys	Asn	Ser	Pro	Tyr	Ile	Val	Gly
	130					135					140				
Phe	Tyr	Gly	Ala	Phe	Tyr	Ser	Asp	Gly	Glu	Ile	Ser	Ile	Cys	Met	Glu
145					150				155					160	
His	Met	Asp	Gly	Gly	Ser	Leu	Asp	Gln	Val	Leu	Lys	Lys	Ala	Gly	Arg
		165					170							175	
Ile	Pro	Glu	Gln	Ile	Leu	Gly	Lys	Val	Ser	Ile	Ala	Val	Ile	Lys	Gly
		180					185						190		
Leu	Thr	Tyr	Leu	Arg	Glu	Lys	His	Lys	Ile	Met	His	Arg	Asp	Val	Lys
	195						200					205			
Pro	Ser	Asn	Ile	Leu	Val	Asn	Ser	Arg	Gly	Glu	Ile	Lys	Leu	Cys	Asp
	210					215					220				
Phe	Gly	Val	Ser	Gly	Gln	Leu	Ile	Asp	Ser	Met	Ala	Asn	Ser	Phe	Val
225					230					235				240	
Gly	Thr	Arg	Ser	Tyr	Met	Ser	Pro	Glu	Arg	Leu	Gln	Gly	Thr	His	Tyr
		245						250						255	
Ser	Val	Gln	Ser	Asp	Ile	Trp	Ser	Met	Gly	Leu	Ser	Leu	Val	Glu	Met
		260					265						270		
Ala	Val	Gly	Arg	Tyr	Pro	Ile	Pro	Pro	Pro	Asp	Ala	Lys	Glu	Leu	Glu

	275					280					285			
Leu	Met	Phe	Gly	Cys	Gln	Val	Glu	Gly	Asp	Ala	Ala	Glu	Thr	Pro
	290					295					300			
Arg	Pro	Arg	Thr	Pro	Gly	Arg	Pro	Leu	Ser	Ser	Tyr	Gly	Met	Asp
305					310					315				320
Arg	Pro	Pro	Met	Ala	Ile	Phe	Glu	Leu	Leu	Asp	Tyr	Ile	Val	Asn
				325					330					335
Pro	Pro	Pro	Lys	Leu	Pro	Ser	Gly	Val	Phe	Ser	Leu	Glu	Phe	Gln
			340					345					350	
Phe	Val	Asn	Lys	Cys	Leu	Ile	Lys	Asn	Pro	Ala	Glu	Arg	Ala	Asp
		355					360					365		Leu
Lys	Gln	Leu	Met	Val	His	Ala	Phe	Ile	Lys	Arg	Ser	Asp	Ala	Glu
370					375						380			Glu
Val	Asp	Phe	Ala	Gly	Trp	Leu	Cys	Ser	Thr	Ile	Gly	Leu	Asn	Gln
385					390			393						Pro
Ser	Thr	Pro	Thr	His	Ala	Ala	Gly	Val						

- (2) INFORMATION FOR SEQ ID NO:12:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 amino acids
- (B) TYPE: peptide
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

				5				10					15	
Met	Leu	Ala	Arg	Arg	Lys	Pro	Val	Leu	Pro	Ala	Leu	Thr	Ile	Asn
			20					25					30	Pro
Thr	Ile	Ala	Glu	Gly	Pro	Ser	Pro	Thr	Ser	Glu	Gly	Ala	Ser	Glu
		35					40					45		Ala
Asn	Leu	Val	Asp	Leu	Gln	Lys	Leu	Glu	Glu	Leu	Glu	Leu	Asp	Glu
	50				55				60					
Gln	Gln	Lys	Lys	Arg	Leu	Glu	Ala	Phe	Leu	Thr	Gln	Lys	Ala	Lys
65				70				75					80	Val
Ser	Glu	Leu	Lys	Asp	Asp	Asp	Phe	Glu	Arg	Ile	Ser	Glu	Leu	Gly
			85					90					95	Ala
Gly	Asn	Gly	Gly	Val	Val	Thr	Lys	Val	Gln	His	Arg	Pro	Ser	Gly
		100						105					110	Leu
Ile	Met	Ala	Arg	Lys	Leu	Ile	His	Leu	Glu	Ile	Lys	Pro	Ala	Ile
	115						120					125		Arg
Asn	Gln	Ile	Ile	Arg	Glu	Leu	Gln	Val	Leu	His	Glu	Cys	Asn	Ser
	130				135					140				Pro
Tyr	Ile	Val	Gly	Phe	Tyr	Gly	Ala	Phe	Tyr	Ser	Asp	Gly	Glu	Ile
145				150					155					160
Ile	Cys	Met	Glu	His	Met	Asp	Gly	Gly	Ser	Leu	Asp	Gln	Val	Leu
			165					170					175	Lys
Glu	Ala	Lys	Arg	Ile	Pro	Glu	Glu	Ile	Leu	Gly	Lys	Val	Ser	Ile
	180						185					190		Ala
Val	Leu	Arg	Gly	Leu	Ala	Tyr	Leu	Arg	Glu	Lys	His	Gln	Ile	Met

Arg	Asp	Val	Lys	Pro	Ser	Asn	Ile	Leu	Val	Asn	Ser	Arg	Gly	Glu	Ile
210						215				220					
Lys	Leu	Cys	Asp	Phe	Gly	Val	Ser	Gly	Gln	Leu	Ile	Asp	Ser	Met	Ala
225					230					235					240
Asn	Ser	Phe	Val	Gly	Thr	Arg	Ser	Tyr	Met	Ala	Pro	Glu	Arg	Leu	Gln
				245					250					255	
Gly	Thr	His	Tyr	Ser	Val	Gln	Ser	Asp	Ile	Trp	Ser	Met	Gly	Leu	Ser
			260					265					270		
Leu	Val	Glu	Leu	Ala	Val	Gly	Arg	Tyr	Pro	Ile	Pro	Pro	Pro	Asp	Ala
		275				280						285			
Lys	Glu	Leu	Glu	Ala	Ile	Phe	Gly	Arg	Pro	Val	Val	Asp	Gly	Glu	Glu
290						295					300				
Gly	Glu	Pro	His	Ser	Ile	Ser	Pro	Arg	Pro	Arg	Pro	Pro	Gly	Arg	Pro
305					310					315					320
Val	Ser	Gly	His	Gly	Met	Asp	Ser	Arg	Pro	Ala	Met	Ala	Ile	Phe	Glu
				325					330					335	
Leu	Leu	Asp	Tyr	Ile	Val	Asn	Glu	Pro	Pro	Pro	Lys	Leu	Pro	Asn	Gly
			340					345					350		
Val	Phe	Thr	Pro	Asp	Phe	Gln	Glu	Phe	Val	Asn	Lys	Cys	Leu	Ile	Lys
			355				360					365			
Asn	Pro	Ala	Glu	Arg	Ala	Asp	Leu	Lys	Met	Leu	Thr	Asn	His	Thr	Phe
			370			375					380				
Ile	Lys	Arg	Ser	Glu	Val	Glu	Glu	Val	Asp	Phe	Ala	Gly	Trp	Leu	Cys
385					390					395					400
Lys	Thr	Leu	Arg	Leu	Asn	Gln	Pro	Gly	Thr	Pro	Thr	Arg	Thr	Ala	Val

2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 668 amino acids

(B) TYPE: peptide

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Glu	Asp	Lys	Phe	Ala	Asn	Leu	Ser	Leu	His	Glu	Lys	Thr	Gly	Lys
			20					25					30		
Ser	Ser	Ile	Gln	Leu	Asn	Glu	Gln	Thr	Gly	Ser	Asp	Asn	Gly	Ser	Ala
			35				40					45			
Val	Lys	Arg	Thr	Ser	Ser	Thr	Ser	Ser	His	Tyr	Asn	Asn	Ile	Asn	Ala
			50			55					60				
Asp	Leu	His	Ala	Arg	Val	Lys	Ala	Phe	Gln	Glu	Gln	Arg	Ala	Leu	Lys
65					70				75					80	
Arg	Ser	Ala	Ser	Val	Gly	Ser	Asn	Gln	Ser	Glu	Gln	Asp	Lys	Gly	Ser
			85					90					95		
Ser	Gln	Ser	Pro	Lys	His	Ile	Gln	Gln	Ile	Val	Asn	Lys	Pro	Leu	Pro
			100				105					110			
Pro	Leu	Pro	Val	Ala	Gly	Ser	Ser	Lys	Val	Ser	Gln	Arg	Met	Ser	Ser

Gln	Val	115	Gln	Ala	Ser	Ser	120	Lys	Ser	Thr	Leu	Lys	125	Asn	Val	Leu	Asp
	130					135						140					
Asn	Gln	Glu	Thr	Gln	Asn	Ile	Thr	Asp	Val	Asn	Ile	Asn	Ile	Asp	Thr		
145					150					155					160		
Thr	Lys	Ile	Thr	Ala	Thr	Thr	Ile	Gly	Val	Asn	Ile	Gly	Leu	Pro	Ala		
				165					170					175			
Thr	Asp	Ile	Thr	Pro	Ser	Val	Ser	Asn	Thr	Ala	Ser	Ala	Thr	His	Lys		
			180					185					190				
Ala	Gln	Leu	Leu	Asn	Pro	Asn	Arg	Arg	Ala	Pro	Arg	Arg	Pro	Leu	Ser		
	195						200					205					
Thr	Gln	His	Pro	Thr	Arg	Pro	Asn	Val	Ala	Pro	His	Lys	Ala	Pro	Ala		
	210					215					220						
Ile	Ile	Asn	Thr	Pro	Lys	Gln	Ser	Leu	Ser	Ala	Arg	Arg	Gly	Leu	Lys		
225					230					235					240		
Leu	Pro	Pro	Gly	Gly	Met	Ser	Leu	Lys	Met	Pro	Thr	Lys	Thr	Ala	Gln		
				245					250					255			
Gln	Pro	Gln	Gln	Phe	Ala	Pro	Ser	Pro	Ser	Asn	Lys	Lys	His	Ile	Glu		
			260					265					270				
Thr	Leu	Ser	Asn	Ser	Lys	Val	Val	Glu	Gly	Lys	Arg	Ser	Asn	Pro	Gly		
	275						280					285					
Ser	Leu	Ile	Asn	Gly	Val	Gln	Ser	Thr	Ser	Thr	Ser	Ser	Ser	Thr	Glu		
	290					295					300						
Gly	Pro	His	Asp	Thr	Val	Gly	Thr	Thr	Pro	Arg	Thr	Gly	Asn	Ser	Asn		
305					310					315					320		
Asn	Ser	Ser	Asn	Ser	Gly	Ser	Ser	Gly	Gly	Gly	Gly	Leu	Phe	Ala	Asn		
			325					330					335				
Phe	Ser	Lys	Tyr	Val	Asp	Ile	Lys	Ser	Gly	Ser	Leu	Asn	Phe	Ala	Gly		
			340					345				350					
Lys	Leu	Ser	Leu	Ser	Ser	Lys	Gly	Ile	Asp	Phe	Ser	Asn	Gly	Ser	Ser		
	355						360					365					
Ser	Arg	Ile	Thr	Leu	Asp	Glu	Leu	Glu	Phe	Leu	Asp	Glu	Leu	Gly	His		
	370					375					380						
Gly	Asn	Tyr	Gly	Asn	Val	Ser	Lys	Val	Leu	His	Lys	Pro	Thr	Asn	Val		
385					390					395					400		
Ile	Met	Ala	Thr	Lys	Glu	Val	Arg	Leu	Glu	Leu	Asp	Glu	Ala	Lys	Phe		
				405					410					415			
Arg	Gln	Ile	Leu	Met	Glu	Leu	Glu	Val	Leu	His	Lys	Cys	Asn	Ser	Pro		
			420					425					430				
Tyr	Ile	Val	Asp	Phe	Tyr	Gly	Ala	Phe	Phe	Ile	Glu	Gly	Ala	Val	Tyr		
	435						440					445					
Met	Cys	Met	Glu	Tyr	Met	Asp	Gly	Gly	Ser	Leu	Asp	Lys	Ile	Tyr	Asp		
	450					455					460						
Glu	Ser	Ser	Glu	Ile	Gly	Gly	Ile	Asp	Glu	Pro	Gln	Leu	Ala	Phe	Ile		
465					470					475					480		
Ala	Asn	Ala	Val	Ile	His	Gly	Leu	Lys	Glu	Leu	Lys	Glu	Gln	His	Asn		
				485					490					495			
Ile	Ile	His	Arg	Asp	Val	Lys	Pro	Thr	Asn	Ile	Leu	Cys	Ser	Ala	Asn		



Gln	Gly	Thr	Val	Lys	Leu	Cys	Asp	Phe	Gly	Val	Ser	Gly	Asn	Leu	Val
		515					520					525			
Ala	Ser	Leu	Ala	Lys	Thr	Asn	Ile	Gly	Cys	Gln	Ser	Tyr	Met	Ala	Pro
	530					535					540				
Glu	Arg	Ile	Lys	Ser	Leu	Asn	Pro	Asp	Arg	Ala	Thr	Tyr	Thr	Val	Gln
545					550					555					560
Ser	Asp	Ile	Trp	Ser	Leu	Gly	Leu	Ser	Ile	Leu	Glu	Met	Ala	Leu	Gly
			565						570						575
Arg	Tyr	Pro	Tyr	Pro	Pro	Glu	Thr	Tyr	Asp	Asn	Ile	Phe	Ser	Gln	Leu
			580					585						590	
Ser	Ala	Ile	Val	Asp	Gly	Pro	Pro	Pro	Arg	Leu	Pro	Ser	Asp	Lys	Phe
		595					600								
Ser	Ser	Asp	Ala	Gln	Asp	Phe	Val	Ser	Leu	Cys	Leu	Gln	Lys	Ile	Pro
	610					615					620				
Glu	Arg	Arg	Pro	Thr	Tyr	Ala	Ala	Leu	Thr	Glu	His	Pro	Trp	Leu	Val
625					630					635					640
Lys	Tyr	Arg	Asn	Gln	Asp	Val	His	Met	Ser	Glu	Tyr	Ile	Thr	Glu	Arg
			645						650					655	
Leu	Glu	Arg	Arg	Asn	Lys	Ile	Leu	Arg	Glu	Arg	Gly	Glu	Asn	Gly	Leu
			660					605			608				
Ser	Lys	Asn	Val	Pro	Ala	Leu	His	Met	Gly	Gly	Leu				

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTAYGGNG CNTTYTTYAT HGA

213

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3636 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATBCTYTCNG GNGCCATKTA

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: peptide

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5 8  
Asp Tyr Lys Asp Asp Asp Asp Lys